# Fig. 1

(78)

```
ATGATGAGCTTTGTGCAAAAGGGGAGCTGGCTACTTCTCGCTCTGCTTCATCCCACTATTATTTTGGCACAACAGGAAGC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 80
TACTACTCGAAACACGTTTTCCCCTCGACCGATGAAGAGCGAGACGAAGTAGGGTGATAATAAAACCGTGTTGTCCTTCG
```

                        ━━━━━ P1 ━━━━▶                                    ━ P3 ━

Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala

```
TGTTGAAGGAGGATGTTCCCATCTTGGTCAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAATATGTG
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 160
ACAACTTCCTCCTACAAGGGTAGAACCAGTCAGGATACGCCTATCTCTACAGACCTTCGGTCTTGGTACGGTTTATACAC
```

━━━ P3 ━━▶

  Val Glu Gly Gly Cys Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Gln Ile Cys

```
TCTGTGACTCAGGATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAACCCAGAAATTCCA
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 240
AGACACTGAGTCCTAGGCAAGAGACGCTACTGTATTATACACTGCTAGTTCTTAATCTGACGGGGTTGGGTCTTTAAGGT
```

         ━━━━ P11-2 ━━━▶

Val Cys Asp Ser Gly Ser Val Leu Cys Asp Asp Ile Ile Cys Asp Asp Gln Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro

```
TTTGGAGAATGTTGTGCAGTTTGCCCACAGCCTCCAACTGCTCCTACTCGCCCTCCTAATGGTCAAGGACCTCAAGGCCC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 320
AAACCTCTTACAACACGTCAAACGGGTGTCGGAGGTTGACGAGGATGAGCGGGAGGATTACCAGTTCCTGGAGTTCCGGG
```

Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro

```
CAAGGGAGATCCAGGCCCTCCTGGTATTCCTGGGAGAAATGGTGACCCTGGTATTCCAGGACAACCAGGGTCCCCTGGTT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 400
GTTCCCTCTAGGTCCGGGAGGACCATAAGGACCCTCTTTACCACTGGGACCATAAGGTCCTGTTGGTCCCAGGGGACCAA
```

                                            ◀━━━ P12 ━━━

Lys Gly Asp Pro Gly Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln Pro Gly Ser Pro Gly

```
CTCCTGGCCCCCCTGGAATCTGTGAATCATGCCCTACTGGTCCTCAGAACTATTCTCCCCAGTATGATTCATATGATGTC
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 480
GAGGACCGGGGGGACCTTAGACACTTAGTACGGGATGACCAGGAGTCTTGATAAGAGGGGTCATACTAAGTATACTACAG
```

                                    ◀━━━ P14 ━━━

Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val

```
AAGTCTGGAGTAGCAGTAGGAGGACTCGCAGGCTATCCT
+----+----+----+----+----+----+----▶ 519
TTCAGACCTCATCGTCATCCTCCTGAGCGTCCGATAGGA
```

                                ◀━━━ P5 ━━━

Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro

# Fig. 2

hP5 : Entire cDNA

| Prepro | Col 1 | Col 3 | Col 2 |
|--------|-------|-------|-------|
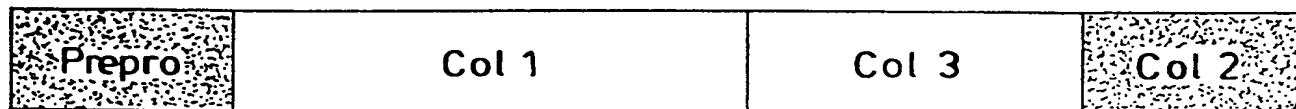
4.5.2 : Mature Monomer

| Col 1 | Col 3 | |
|-------|-------|---|

ne6 : Deletion Mutant

| Col 1 | Col 3 | |
|-------|-------|---|

2.8.6 : Col 2 Deletion Mutant

| Col 1 | Col 3 |
|-------|-------|

# Fig. 3



conc. PIIINP ng/mL
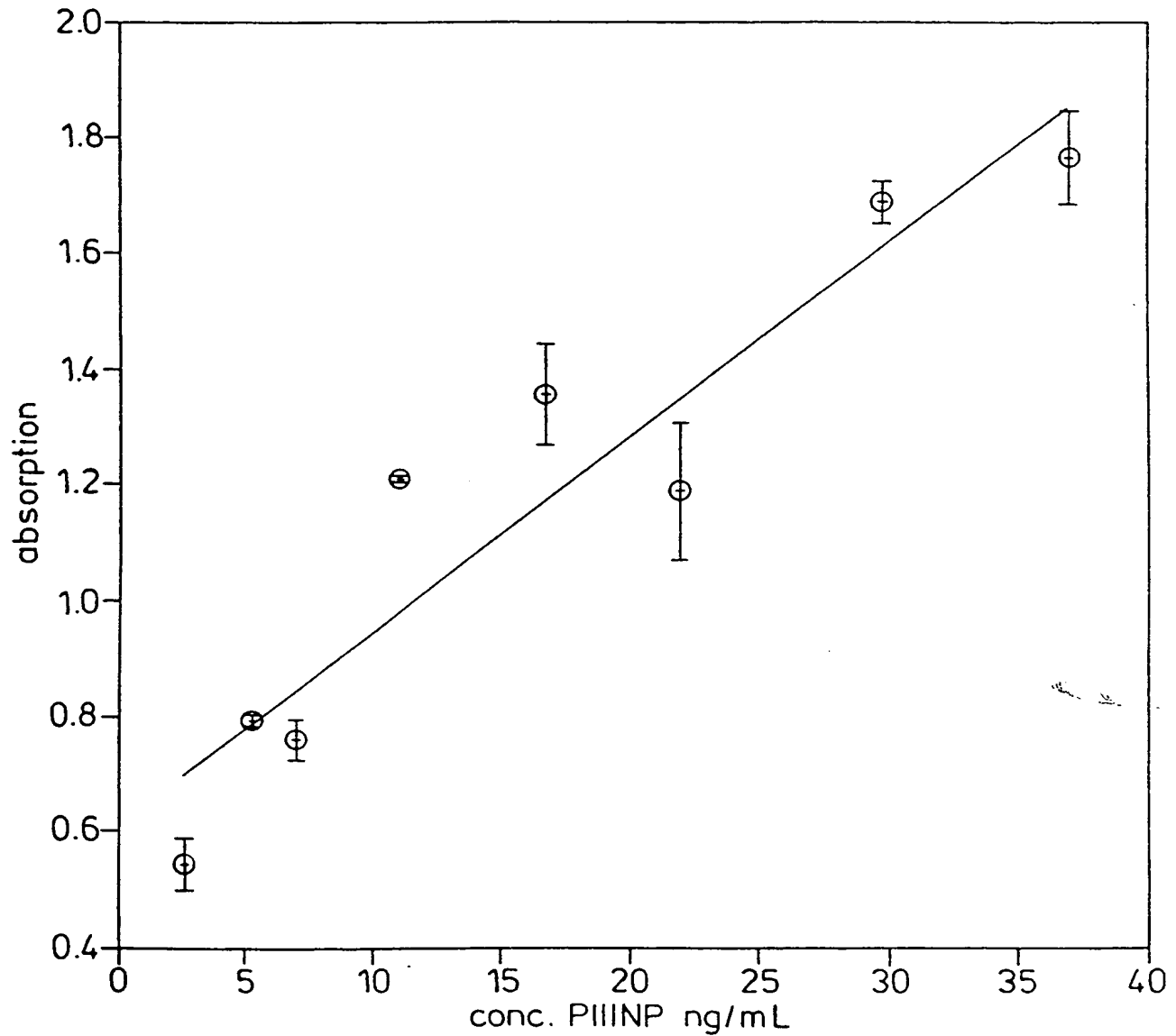
⊕   conc.PIIINP v absorp.
——   regression line

# Fig. 4